



A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A;Reference number: A53598; MUID:94216359  
A;Accession: A53598  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 234-251 <KIM>  
C;Comment: The a allele sequence is shown.

C;Genetics:  
A;Introns: 138/1; 236/1; 258/1; 368/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ<sub>λ</sub>) chains and two heavy (μ) chains. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F;157-222/Domain: immunoglobulin homology <IM1>  
F;236-257/Region: hinge  
F;283-350/Domain: immunoglobulin homology <IM2>  
F;387-454/Domain: immunoglobulin homology <IM3>  
F;152/Disulfide bonds: interchain (to light chain) #status predicted  
F;164-220, 288-348, 394-452/Disulfide bonds: interchain (to heavy chain) #status predicted  
F;247, 250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.1%; Score 2190.5; DB 1; Length 474;  
Best Local Similarity 91.2%; Pred. No. 4.1e-123;  
Matches 415; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

Qy 1 EVOLQOOSGPVELVKPGASVMSICRSTSAYTENTVWVKOSHGESLEWIGGINPYGGSF 60  
Db 20 EVOLQOOSGPVELVKPGASVMSICRSTSAYTENTVWVKOSHGESLEWIGGINPYGGSF 79

Qy 61 SPKFKGKATLTVDKSSSTAYMLSLTSEDSAVYCA--RRAGAYFDWGQGQTTLVSS 118  
Db 80 NEFKFGKATLTVDKSSSTAYMLSLTSEDSAVYCA--RRAGAYFDWGQGQTTLVSSA 139

Qy 119 AKTTPSVYPLAPSGCGDTGSSVYLGLKYGFPESVTWTNSCSLSSSYHTTPALQSG 178  
Db 140 AKTTPSVYPLAPSGCGDTGSSVYLGLKYGFPESVTWTNSCSLSSSYHTTPALQSG 199

Qy 179 LYTMSSSVTVPSSWPSQTVTCVAHPASSTTVKLEPSPGILSTINOPCPCKCHKCPA 238  
Db 200 LYTMSSSVTVPSSWPSQTVTCVAHPASSTTVKLEPSPGILSTINOPCPCKCHKCPA 259

Qy 239 PNLEGGPSVFTFPNNIKDVIMIISLTPKVCVVVDYSEDDPDVQTSWFVNNEVHTAQQT 298

Db 260 PNLEGGPSVFTFPNNIKDVIMIISLTPKVCVVVDYSEDDPDVQTSWFVNNEVHTAQQT 319

Qy 299 HREDINSTRVWSTUPIQHODWMSGKEFKCKVNKKDLSPIERTISKIGLVRAPQVIL 358

Db 320 HREDINSTRVWSTUPIQHODWMSGKEFKCKVNKKDLSPIERTISKIGLVRAPQVIL 379

Qy 359 PPAEQLRSKDSVSLTCIUVGFNPQDISVEMTSNGHTEENYKDAPVLDSDGSPYIYSKLN 418

Db 380 SPPPEQLRSKDSVSLTCIUVGFNPQDISVEMTSNGHTEENYKDAPVLDSDGSPYIYSKLN 439

Qy 419 MTKSWEKTDFFSCNVRHREGLKNYLKKTISRSPGK 454

Db 440 MTKSWEKTDFFSCNVRHREGLKNYLKKTISRSPGK 475

RESULT 3  
S01321  
Ig gamma-2b chain precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Accession: S01321  
C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
C;Reference number: S01321  
R;Ducane, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A;Reference number: S37483  
A;Accession: S37483  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-469 <DUC>  
A;Cross-references: EMBL:X70423; NID:9406252; PID:CAA49868.1; PID:9406253  
C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>  
C;Keywords: immunoglobulin F;276-345/Domain: immunoglobulin homology <IMM>

Query Match 73.8%; Score 1835; DB 2; Length 469;  
Best Local Similarity 75.7%; Pred. No. 5.3e-102;  
Matches 345; Conservative 44; Mismatches 59; Indels 8; Gaps 3;

Qy 1 EVOLQOOSGPVELVKPGASVMSICRSTSAYTENTVWVKOSHGESLEWIGGINPYGGSF 60  
Db 20 QIOLQQSGPVELVKPGASVMSICRSTSAYTENTVWVKOSHGESLEWIGGINPYGGSF 79



QY 119 AKTTPPSVNPPLAPGGDTGSSVTLGLVKGYFPESTVTWNSSSLSSSVHTPAULQSG 178  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
 Db 1 AKTTPPSVNPPLAPGGDTGSSVTLGLVKGYFPESTVTWNSSSLSSSVHTPAULQSG 60

QY 179 LYTMSSSVTPSSTWPSPQTVCYAHASSTTVPKLEPLSGP1STINPCCPKCHKCPA 238  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
 Db 61 LYTMSSSVTPSSTWPSPQTVCYAHASSTTVPKLEPLSGP1STINPCCPKCHKCPA 120

QY 239 PNLEGGPSVYIFPPNIKDVM1STTPKVCTVWVWSEDDPDQ1SWFVNNEVHTAQQT 298  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
 Db 121 PNLEGGPSVYIFPPNIKDVM1STTPKVCTVWVWSEDDPDQ1SWFVNNEVHTAQQT 180

RESULT 6

PC44316 monoclonal antibody 13-1 heavy chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Accession: PC44316

C;Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000

R;Akashi, S.; Kato, K.; Toriawa, T.; Dohmae, N.; Yamaguchi, H.; Kanachi, M.; Harada, A.

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin

A;Reference number: JCS310; MUID:98063277

A;Accession: PC44316

A;Molecule type: protein

A;Residues: 1-444 <AKA>

C;Comment: this catalytic antibody has peroxidase oxidase activity. It is directed again F;221-320(Domain: immunoglobulin homology <IM>  
 F;99;Disulfide bonds: interchain (to 98) #status predicted  
 F;99;Disulfide bonds: interchain (to 109) #status predicted

Query Match 57.9%; score 1439; DB 2; Length 444;  
 Best Local Similarity 59.3%; Pred. No. 1.7e-78;  
 Matches 271; Conservative 68; Mismatches 102; Indels 16; Gaps 6;

QY 1 EVQLQSQGPVELVKPGASMWSICRTSAYFTENTVHWVKOSHGESELWIGI--NPyTGG 57  
 |||| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 1 EVQKETGGVLGVRLRNLKLSCLSLGEFTSNRYHHLRQPGKAKEWIAVITYKSDNYGA 60

QY 58 SIFSKFKATLVDKESSTAYMELRSITSEDAVYCARAGAYYEWGQGTLLTVS 117  
 |||| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 61 K-YAESVRGRETISRRDKSSKSVVQIOMNRREEDTAYYCCTPWYAMDCWGQTSVIVS 119

QY 118 SAKTTPPSVYPLAGCGGDTGTSSVTLGLVKGYFPESTVTWNSSGLSSSVHTPAULQSG 177  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
 Db 120 SAKTTPPSVYPLAGCGGDTGTSSVTLGLVKGYFPESTVTWNSSGLSSSVHTPAULQSG 179

QY 178 GLYIMSSSVTPSSTWPSPQTVCYAHASSTTVPKLEPLSGP1STINPCCPKCHKCPA 237  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
 Db 180 DLYTFLSSVTPSSTWPSPQTVCYAHASSTTVPKLEPLSGP1STINPCCPKCHKCPA 230

QY 238 APNIEEGGSVPIFPNIKDVM1STTPKVCTVWVWSEDDPDQ1SWFVNNEVHTAQQT 297  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
 Db 231 VPEVS--SVFIFPKPKVLTILTPKTCVWVWSEDDPDQ1SWFVNNEVHTAQQT 287

QY 298 THRDYNSTRVSTLPTOHODWNGSKERKCKVWNKDLSPERTISKIKGLYRAPQYI 357  
 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||  
 Db 288 PREQQFNSTRSVSELPIMHQDWLNGKEFCKCRVNSAAFPAPIERTISKIKGRPKAPQYI 347

RESULT 7

G2MSA Ig gamma-2a chain C region, secreted form (allele a) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1980 #sequence\_revision 01-Sep-1981 #text\_change 16-Jun-2000

C;Accession: A02152; A32657; A32658

R;Slkorov, J.L.; Aufray, C.; Rougeon, F.

Nucleic Acids Res. 8, 3143-3155, 1980

A;Title: Structure of the constant and 3' untranslated regions of the murine Balb/c g

A;Reference number: A02152; MUID:81076554

A;Accession: A02152

A;Molecule type: mRNA

A;Residues: 1-330 <SIK>

A;Cross-references: GB:00798; NID:951835; PIDN:CAA24178.1; PID:91333984

R;Yamawaki-Karaoka, Y.; Miyata, T.; Honjo, T.

Nucleic Acids Res. 9, 1365-1381, 1981

A;Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and

A;Reference number: A32657; MUID:81198976

A;Molecule type: DNA

A;Residues: 1-330 <YAM>

A;Cross References: GB:100470

A;Note: the sequence was determined from the germline gene

R;Ollio, R.; Aufray, C.; Morchamps, C.; Rougeon, F.

Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 1981

A;Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggest

A;Reference number: A32658; MUID:81223894

A;Accession: A32658

A;Molecule type: DNA

A;Residues: 1-330 <OLL>

A;Note: the sequence was determined from the germline gene

A;Note: Lys-330 is removed posttranslationally

R;Bourgois, A.; Fougerousse, M.; Rocca-Serra, J.

Eur. J. Biochem. 43, 43-45, 1974

A;Title: Determination of the primary structure of a mouse IgG2a immunoglobulin: amino acid sequence annotation

A;Reference number: A32659; MUID:73056887

A;Contents: annotation: myeloma protein MOPC 173

A;Note: this is one paper in a series reporting the sequence; for additional references see below

A;Note: this sequence differs from that shown at a number of positions

R;de Preval, C.; Fougerousse, M.

Eur. J. Biochem. 30, 452-462, 1972

A;Title: Determination of the primary structure of a mouse IgG2a immunoglobulin. I

A;Reference number: A32660; MUID:73056887

A;Contents: annotation: MOPC 173, disulfide bonds

C;Genetics:

A;Introns: 1/1; 98/1; 114/1; 224/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology <IM>

C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl

F;20-84(Domain: immunoglobulin homology <IM> hinge

F;98-113(Domain: hinge

F;137-206(Domain: immunoglobulin homology <IM>

F;243-310(Domain: immunoglobulin homology <IM>

F;25-Disulfide bonds: interchain (to light chain) #status experimental

F;27-82,14-204,250-308(Disulfide bonds: #status experimental

F;107,110,112(Disulfide bonds: interchain (to heavy chain) #status experimental

F;180(Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.1%; Score 1419; DB 1; Length 330;  
 Best Local Similarity 78.6%; Pred. No. 1.8e-77;  
 Matches 264; Conservative 30; Mismatches 36; Indels 6; Gaps 2;

QY 119 AKTTPPSVYPLARGCGDPTGSSVTLGCLVKGYFPESVTVWNSGSUSSSVHFPALQSG 178  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 1 AKTTPPSVYPLARGCGDPTGSSVTLGCLVKGYFPESVTVWNSGSUSSSVHFPALQSG 60

QY 179 LYMMSSVTVPSTWPSSOTVTCVAHPASSTKVDKIEPSPGPISTINRCPCKECHCPA 238  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 61 LYTTSSSVTVPSTWPSSOTCVAHPASSTKVDKIEPSPGPISTINRCPCKECHCPA 238

QY 239 PNLEGGPSVFIPPNPKDVLMISLPIKUTCVVWDVSEDDPDQIISWIVNNVEHTAQOT 298  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 115 PNLEGGPSVFIPPNPKDVLMISLPIKUTCVVWDVSEDDPDQIISWIVNNVEHTAQOT 174  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 115 PNLEGGPSVFIPPNPKDVLMISLPIKUTCVVWDVSEDDPDQIISWIVNNVEHTAQOT 298

QY 299 HREDYNSTIRVSTLPIOHQDWGSKERCKVNNKDLSPPIERTISKGLYRAPQVIL 358  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 175 HREDYNSTIRVSTLPIOHQDWGSKERCKVNNKDLSPPIERTISKGLYRAPQVIL 234

QY 359 PPPEEQLSRKDVSITCLVYNGPDISWETSNGHTEENYKOPAPVLDGSYFYIYKLN 418  
 ||||| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 235 PPPEEQLSRKDVSITCLVYNGPDISWETSNGHTEENYKOPAPVLDGSYFYIYKLN 294

QY 419 MKSKWEKTDSCSNVRLEGKLYKLTISRPGK 454  
 :: :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 295 VERKNWERNYSCSVVHEGLAHHTKSFRTPG 330

## RESULT 8

GMSAM

Ig gamma-2a chain C region, membrane-bound form - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Feb-1994 #sequence\_revision 31-Mar-1991 #text\_change 16-Jul-1999

C;Accession: A02154; B32657; I57809

C;Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982

A;Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin

A;Reference number: A02154; MUID:82222190

A;Accession: A02154

A;Molecule type: DNA

A;Residues: 329-399 &lt;AM&gt;

A;Cross-references: GB:J00471

A;Note: the sequence was determined from the germline gene

R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.

R;Nucleic Acids Res. 9, 1365-1381, 1981

A;Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and env

A;Reference number: A32657; MUID:81198976

A;Accession: B32657

A;Molecule type: DNA

A;Residues: 1-329, 'K' &lt;YA2&gt;

R;Hall, B.; Milcarek, C.

R;Mol. Immunol. 26, 819-826, 1989

A;Title: Sequence and polyadenylation site determination of the murine immunoglobulin ga

A;Reference number: 157809; MUID:90097953

A;Accession: I57809

A;Title: Preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 373-399 &lt;RBS&gt;

A;Cross-references: GB:M3532; PID:9194478; PID:AAA37919\_1; PID:9387217  
 A;Reference number: 157809; MUID:90097953  
 A;Accession: I57809  
 A;Title: Preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-335 &lt;SCH&gt;

A;Cross-references: GB:J00479

Best Local Similarity 78.5%; Pred. No. 4.6e-77; Indels 6; Gaps 2;  
 Matches 263; Conservative 30; Mismatches 36;

QY 119 AKTTPPSVYPLARGCGDPTGSSVTLGCLVKGYFPESVTVWNSGSUSSSVHFPALQSG 178  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 1 AKTTPPSVYPLARGCGDPTGSSVTLGCLVKGYFPESVTVWNSGSUSSSVHFPALQSG 60

QY 179 LYMMSSVTVPSTWPSSOTVTCVAHPASSTKVDKIEPSPGPISTINRCPCKECHCPA 238  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 61 LYTTSSSVTVPSTWPSSOTCVAHPASSTKVDKIEPSPGPISTINRCPCKECHCPA 238

QY 239 PNLEGGPSVFIPPNPKDVLMISLPIKUTCVVWDVSEDDPDQIISWIVNNVEHTAQOT 298  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 115 PNLEGGPSVFIPPNPKDVLMISLPIKUTCVVWDVSEDDPDQIISWIVNNVEHTAQOT 174  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 115 PNLEGGPSVFIPPNPKDVLMISLPIKUTCVVWDVSEDDPDQIISWIVNNVEHTAQOT 298

QY 299 HREDYNSTIRVSTLPIOHQDWGSKERCKVNNKDLSPPIERTISKGLYRAPQVIL 358  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 175 HREDYNSTIRVSTLPIOHQDWGSKERCKVNNKDLSPPIERTISKGLYRAPQVIL 234

QY 359 PPPEEQLSRKDVSITCLVYNGPDISWETSNGHTEENYKOPAPVLDGSYFYIYKLN 418  
 ||||| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 235 PPPEEQLSRKDVSITCLVYNGPDISWETSNGHTEENYKOPAPVLDGSYFYIYKLN 294

QY 419 MKSKWEKTDSCSNVRLEGKLYKLTISRPGK 454  
 :: :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 295 VERKNWERNYSCSVVHEGLAHHTKSFRTPG 329

## RESULT 9

G2MSAB

Ig gamma-2a chain C region, secreted form (allele b) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 16-Jul-1999

C;Accession: A02153; A32656

R;Schreier, P.H.; Bothwell, A.L.M.; Mueller-Hill, B.; Baltimore, D.

R;Proc. Natl. Acad. Sci. U.S.A. 78, 4495-4499, 1981

A;Title: Multiple differences between the nucleic acid sequences of the IgG2a(a) and

A;Reference number: A02153; MUID:82037861

A;Accession: A02153

A;Molecule type: mRNA

A;Residues: 1-335 &lt;SCH&gt;

A;Cross-references: GB:J00479

A;Experimental source: strain C57BL/6

R;Boggs, M.J.; Lauwerys, M.; Strosberg, A.D.

R;Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981

A;Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc reg

A;Reference number: A32656; MUID:82037777

A;Accession: A32656

A;Molecule type: Protein

A;Residues: 118-267, 'E', 269-328, 'G', 330-334 &lt;DOG&gt;

A;Title: Sequence and polyadenylation site determination of the murine immunoglobulin ga

A;Reference number: 157809; MUID:90097953

A;Accession: I57809

A;Title: Preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 373-399 &lt;RBS&gt;

A;Cross-references: GB:M3532; PID:9194478; PID:AAA37919\_1; PID:9387217  
 A;Reference number: 157809; MUID:90097953  
 A;Accession: I57809  
 A;Title: Preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-335 &lt;SCH&gt;

A;Cross-references: GB:J00479

Best Local Similarity 78.5%; Pred. No. 4.6e-77; Indels 6; Gaps 2;  
 Matches 263; Conservative 30; Mismatches 36;

QY 119 AKTTPPSVYPLARGCGDPTGSSVTLGCLVKGYFPESVTVWNSGSUSSSVHFPALQSG 178  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 1 AKTTPPSVYPLARGCGDPTGSSVTLGCLVKGYFPESVTVWNSGSUSSSVHFPALQSG 60

QY 179 LYMMSSVTVPSTWPSSOTVTCVAHPASSTKVDKIEPSPGPISTINRCPCKECHCPA 238  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 61 LYTTSSSVTVPSTWPSSOTCVAHPASSTKVDKIEPSPGPISTINRCPCKECHCPA 238

QY 239 PNLEGGPSVFIPPNPKDVLMISLPIKUTCVVWDVSEDDPDQIISWIVNNVEHTAQOT 298  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 115 PNLEGGPSVFIPPNPKDVLMISLPIKUTCVVWDVSEDDPDQIISWIVNNVEHTAQOT 174  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 115 PNLEGGPSVFIPPNPKDVLMISLPIKUTCVVWDVSEDDPDQIISWIVNNVEHTAQOT 298

QY 299 HREDYNSTIRVSTLPIOHQDWGSKERCKVNNKDLSPPIERTISKGLYRAPQVIL 358  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 175 HREDYNSTIRVSTLPIOHQDWGSKERCKVNNKDLSPPIERTISKGLYRAPQVIL 234

QY 359 PPPEEQLSRKDVSITCLVYNGPDISWETSNGHTEENYKOPAPVLDGSYFYIYKLN 418  
 ||||| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 235 PPPEEQLSRKDVSITCLVYNGPDISWETSNGHTEENYKOPAPVLDGSYFYIYKLN 294

QY 419 MKSKWEKTDSCSNVRLEGKLYKLTISRPGK 454  
 :: :||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 295 VERKNWERNYSCSVVHEGLAHHTKSFRTPG 329

## Query Match

Best Local Similarity

77.1%

Score

1305.5

DB

1

Length

335

Matches

259

Conservative

33

MisMatches

43

Indels

1

Gaps

1

F137-206/Domain: immunoglobulin homology &lt;IMM&gt;

F136-363/Domain: transmembrane #status predicted &lt;TM&gt;

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin C region; immunoglobulin homology &lt;IM&gt;

C;Genetics: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl

C;Introns: 1/1; 114/1; 224/1; 329/1; 372/1

C;Comment: The sequence of residues 1-328 was assumed to be identical with the correspon

C;hat it contains an alternative 3' end, encoded in separate exons, that is homologous wit

C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl

C;Domain: immunoglobulin homology &lt;IM&gt;

F136-363/Region: hinge

C;Superfamily: immunoglobulin C region; immunoglobulin homology &lt;IM&gt;

F142-211/Domain: immunoglobulin homology &lt;IM&gt;

F140-315/Domain: immunoglobulin homology &lt;IM&gt;

F140-315/Region: hinge

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin C region; immunoglobulin homology &lt;IM&gt;

F180/Binding site: carbohydrate (Asn) (covalent) #status predicted

C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl

F180/Domain: intracellular #status predicted &lt;INT&gt;

F180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity

77.1%

Pred. No.

1.8e-75

Matches

259

Conservative

33

MisMatches

43

Indels

1

Gaps

1

F137-206/Domain: immunoglobulin homology &lt;IM&gt;

F136-363/Domain: transmembrane #status predicted &lt;TM&gt;

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin C region; immunoglobulin homology &lt;IM&gt;

F142-211/Domain: immunoglobulin homology &lt;IM&gt;

F140-315/Domain: immunoglobulin homology &lt;IM&gt;

F140-315/Region: hinge

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin C region; immunoglobulin homology &lt;IM&gt;

F180/Binding site: carbohydrate (Asn) (covalent) #status predicted

F180/Domain: intracellular #status predicted &lt;INT&gt;

F180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity

77.1%

Pred. No.

1.8e-75

Matches

259

Conservative

33

MisMatches

43

Indels

1

Gaps

1

F137-206/Domain: immunoglobulin homology &lt;IM&gt;

F136-363/Domain: transmembrane #status predicted &lt;TM&gt;

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin C region; immunoglobulin homology &lt;IM&gt;

F142-211/Domain: immunoglobulin homology &lt;IM&gt;

F140-315/Domain: immunoglobulin homology &lt;IM&gt;

F140-315/Region: hinge

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin C region; immunoglobulin homology &lt;IM&gt;

F180/Binding site: carbohydrate (Asn) (covalent) #status predicted

F180/Domain: intracellular #status predicted &lt;INT&gt;

F180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity

77.1%

Pred. No.

1.8e-75

Matches

259

Conservative

33

MisMatches

43

Indels

1

Gaps

1

F137-206/Domain: immunoglobulin homology &lt;IM&gt;

F136-363/Domain: transmembrane #status predicted &lt;TM&gt;

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin C region; immunoglobulin homology &lt;IM&gt;

F142-211/Domain: immunoglobulin homology &lt;IM&gt;

F140-315/Domain: immunoglobulin homology &lt;IM&gt;

F140-315/Region: hinge

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kar

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin C region; immunoglobulin homology &lt;IM&gt;

F180/Binding site: carbohydrate (Asn) (covalent) #status predicted

F180/Domain: intracellular #status predicted &lt;INT&gt;

F180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity

77.1%

Pred. No.

1.8e-75

Matches

QY	179 LYIMSSSTVTPSSWPSQTVCVAHAPASSTDVKLLEPSPGSTINTCOPPCRECHKCPA	238	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK	454
QY	111:1111:1111:1111:1111:1111:1111:1111:1111:1111:1111:1111:1111:	119	1::1:	333
Db	61 LYLTSSSTVTPSNTTICVWPAHAPASSTDVKLLEPSPGSTINTCOPPCRECHKCPA	119	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	239 PNLEGGPSVFIFPPNPKDVLMSLTPKTCVWVDVSSEDDPDVQISMWVNNEVHTAQTO	298	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	120 PDLLGGPSVFIFPPKIKVLMISLSPMTCVWVDVSSEDDPDVQISMWVNNEVHTAQTO	179	QY	1::1:
QY	299 HREDYNSTIRVSTLPTQHQDMGKPFCKVNNKDLSPPIERTISKIGLVRAPOVIL	358	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
Db	180 HREDYNSTIRVSVSALPQHQDMGKPFCKVNNKDLSPPIERTISKIGLVRAPOVIL	239	QY	359 PPAEQOLRSKDVSLTCIWLGVFGNPGDISWEWTSGHTEENYKDAPVLDGSFVIYSKLN
QY	1111:1111:1111:1111:1111:1111:1111:1111:1111:1111:1111:1111:1111:	418	Db	240 PPPAEEMTKFSLSLTCMTCFLPRAEIAVWTNSGRTEQYKNATVLDSDGSYFMSKL
Db	240 PPPAEEMTKFSLSLTCMTCFLPRAEIAVWTNSGRTEQYKNATVLDSDGSYFMSKL	299	QY	419 MKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
QY	300 VOKSTWERGSSLFACSVWHEVLNLHLLTITKISRIGK 335	454	QY	419 MKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
RESULT	10		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
PS0018	Ig gamma-2b chain C region - rat		QY	1::1:
C.Species:	Rattus norvegicus (Norway rat)		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
Date:	07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
C.Accession:	PS0018; B25941		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
R.Bruedegemann,	M.		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Gene 74, 473-482, 1988			Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
A.Title:	Evolution of the rat immunoglobulin gamma heavy-chain gene family.		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
A.Reference number:	PS0017; MUID:89232738		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
A.Molecule type:	DNA		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
A.Residues:	1-333  		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
R.Bruedegemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.			QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Proc. Natl. Acad. Sci. U.S.A. 83, 605-6079, 1986			Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
A.Title:	Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody genes		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
A.Reference number:	A25941; MUID:86287397		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
A.Status:	preliminary		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
A.Molecule type:	DNA		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
A.Residues:	227-333  		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
C.Genetics:			Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
A.Introns:	96/1; 117/1; 227/1		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
C.Superfamily:	immunoglobulin C region; immunoglobulin homology		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
C.Keywords:	immunoglobulin		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
F;20-82/Domain:	immunoglobulin homology <IMM>		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
Query Match	53.3%; Score 1326.5; DB 2; Length 333;		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Best Local Similarity	73.6%; Pred. No. 5; 8e-72;		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
Matches	248; Conservative		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Matches	248; Conservative		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	119 AKITPPSVYPLARGCGDTGSSVTLGCLVKGYFPESTVVTWNSGSLSSVHTRPALLQG	178	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	1 AQTATPSVYPLARGCGDTGSSVTLGCLVKGYFPESTVVTWNSGALSSVHTRPALLQG	178	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	179 LXTMSSSTVTPSNTWPSOTVCSVVAHAPASSTDVKLLEPSPGSTINTCOPPCRECHKCP	237	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	1 AQTATPSVYPLARGCGDTGSSVTLGCLVKGYFPESTVVTWNSGALSSVHTRPALLQG	60	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	61 LXTLTTSSVYPLSTWPSQTVCVVAHAPASSTDVKLLEPSPGSTINTCOPPCRECHKCP	116	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	1 LXTLTTSSVYPLSTWPSQTVCVVAHAPASSTDVKLLEPSPGSTINTCOPPCRECHKCP	116	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	238 APNLEGGPSVFIFPPNPKDVLMSLTPKTCVWVDVSSEDDPDVQISMWVNNEVHTAQTO	297	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	117 VPELLGGSVVFIFPPKPKDILJLISQNAKVTCVWVDVSSEDDPDVQISMWVNNEVHTAQTO	176	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	298 THREDYNSTIRVSTLPTQHQDMGKPFCKVNNKDLSPPIERTISKIGLVRAPOVIL	357	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	177 PREEQQNSTFRVSVSALPQHQDMGKPFCKVNNKDLSPPIERTISKIGLVRAPOVIL	236	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	358 LPPPABOLSKRKVSVLCLVVGNGPDSWEMTSNGHFEENYKDAPVLDGSDESYFYSKL	417	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	237 MGPPTEDTLTQPSVLSLCTGSLPNDGEGVWNSHTEKVKNPTEPMDSDFESWML	296	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	239 PNLEGGPSVFIFPPNPKDVLMSLTPKTCVWVDVSSEDDPDVQISMWVNNEVHTAQTO	297	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	120 PDLLGGPSVFIFPPKIKVLMISLSPMTCVWVDVSSEDDPDVQISMWVNNEVHTAQTO	179	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	299 HREDYNSTIRVSTLPTQHQDMGKPFCKVNNKDLSPPIERTISKIGLVRAPOVIL	358	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	180 HREDYNSTIRVSVSALPQHQDMGKPFCKVNNKDLSPPIERTISKIGLVRAPOVIL	239	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	359 PPAEQOLRSKDVSLTCIWLGVFGNPGDISWEWTSGHTEENYKDAPVLDGSFVIYSKLN	418	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	240 PPPAEEMTKFSLSLTCMTCFLPRAEIAVWTNSGRTEQYKNATVLDSDGSYFMSKL	299	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	419 MKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK	454	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	300 VOKSTWERGSSLFACSVWHEVLNLHLLTITKISRIGK 335	454	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
RESULT	10		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
PS0018	Ig gamma-2b chain C region - rat		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
C.Species:	Rattus norvegicus (Norway rat)		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Date:	07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
C.Accession:	PS0018; B25941		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
R.Bruedegemann,	M.		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Gene 74, 473-482, 1988			Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
A.Title:	Evolution of the rat immunoglobulin gamma heavy-chain gene family.		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
A.Reference number:	PS0017; MUID:89232738		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
A.Molecule type:	DNA		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
A.Residues:	1-333  		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
R.Bruedegemann, M.; Free, J.; Diamond, A.; Cobbold, S.; Waldmann, H.			QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Proc. Natl. Acad. Sci. U.S.A. 83, 605-6079, 1986			Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
A.Title:	Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody genes		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
A.Reference number:	A25941; MUID:86287397		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
A.Status:	preliminary		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
A.Molecule type:	DNA		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
A.Residues:	227-333  		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
C.Genetics:			Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
A.Introns:	96/1; 117/1; 227/1		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
C.Superfamily:	immunoglobulin C region; immunoglobulin homology		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
C.Keywords:	immunoglobulin		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
F;20-82/Domain:	immunoglobulin homology <IMM>		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
Query Match	53.1%; Score 1321.5; DB 2; Length 472;		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Best Local Similarity	54.8%; Pred. No. 1.7e-71;		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
Matches	255; Conservative		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Matches	255; Conservative		Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	1 EVOLQOSGPBLVKPGAVSMCRSTSAYTENTWVWKOSHGESTIEWIGINPYGSIF	60	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	18 QVRQESQGPGLATIQLTISVTCITSGFSUNNYGVWWRQAPGKALEFWLGG-SGFDDEDIO	76	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	61 SPKFFKGAKTHVDKSSVASTMELNSLTSEDSAVYCAR-----RAGAY-YFDWQGQT	113	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	77 NPVLKSLSLTKDSSKQSLSLTSIVTIEDAVYCARYDSSHAFAVASYDFWGPGLL	136	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	114 LTVSSAKTTPSVYPLAPCGCGDTGSSVTLGCLVKGYFPESTVVTWNSGSLSSVHTRPALLQ	173	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	137 ISVLASTTIPPKVPLTSCGDTSSIVTIVLGCLVKGYFPESTVVTWNSGALTSVHFTPE	196	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	174 LLQSGLYMSSSTVPSSTWPSQTVCVAHAPASSTDVKLLEPSPGSTINTCOPPCRECHKCP	231	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	197 ILQSSGLYLSLSSVWVTPASGQFOTICVNAHAPASSTDVKLLEPSPGSTINTCOPPCRECHKCP	248	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	232 ECHKCPAPNLEGGPSVFIFPPNPKDVLMSLTPKTCVWVDVSSEDDPDVQISMWVNNEV	291	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	308 RTARKPKEOFNSFRVSVSALPQHQDMGKPFCKVNNKDLSPPIERTISKIGLVRAPOVIL	367	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	352 APOVILPPPAEIQSRKDVSLTCIWLGVFGNPGDISWEWTSGHTEENYKDAPVLDSDG	409	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	368 EPQVYLAPQPEEKSLSLTSIVTIVLGCLVKGYFPESTVVTWNSGALSSDVFHPPAVLOG	409	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
QY	410 SYFTYKLNMTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK	454	QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
Db	428 SYFLYSLRLVDKNSWQEGDYTACVWMEHALHNHYQKTSKPPG	472	Db	297 NVERSRWDSDRAPEVCSVHESGLHNHHVEKSISRPGK
RESULT	12		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
S22080	Ig heavy chain precursor (B/NT.4A.17.H5.A5) - bovine		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
N;Alternate names:	Ig gamma-1 chain C region (clone 8.10)		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
C.Species:	Bos primigenius taurus (cattle)		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
C.Date:	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
C.Accession:	S22080; 506610; A3103		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
R;Senders:	P. G.		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
submitted to the EMBL Data Library, November 1991			QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK
A;Reference number:	S22080		QY	418 NMKTSKWEKTDPSFCNRHEGCKNYLKTTISRSPGK

A; Status: preliminary  
A; Molecule type: mRNA  
A; Residues: 1-470 <SAN>  
A; Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440  
R; Simmons, D.B.A.; Clarkson, C.A.; Beale, D.  
Mol. Immunol. 26, 841-850, 1989  
A; Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2B/Domains: immunoglobulin homology <IMM>  
A; Accession: S06610; MUID:90097956  
A; Residues: 142-470 <SYN>  
A; Cross-references: EMBL:X16701  
A; Note: the sequence was determined from the germline gene  
C; Genetics:  
A; Gene: Ig CH gamma-1  
A; Introns: 97/1; 111/1; 221/1  
C; Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>  
C; Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
F; 161-225/Domain: immunoglobulin homology <IMM>  
F; 318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.7%; Score 1286.5; DB 2; Length 470;  
Best local Similarity 54.2%; Pred. No. 2.1e-69; Mismatches 8;  
Matches 231; Conservative 70; Indels 21; Gaps 8;

Qy 1 EVQLQSQPELVLKRGASMISCRISAYTFTENVWVHQSHGESELEWIGGINPYGSIF 60  
Db 20 QVQIRESGPSLVKPSQTSLTCTVSGFSLSYSSVPIEDTATVWVHQAPGKALERNVGGTS-GGTTYY 78

Qy 61 SPKFKGKATLTVDKSSTAYMELRSLSEDSAVYCARA-----GAYYFDWVQGQTL 114  
Db 79 NPALKSRISITKENSQVSLSVSSVPIEDTATVYCARSTYGVGDSA-LADAWGQSLV 137

Qy 115 TVSSAKTTPPSVYPLAPCGDITGSSVNLKGYPPESVTVWNSGLSSVHTPAL 174  
Db 138 TVSSASTIATPKVYPLPSSCCGDKSSVTPLGCLSSYMPPEPVTVWNSGALKSGVHTFPV 197

Qy 175 LQ-SGLYMSSTSVTYPSPSTWPSTVPTVVAHPASSTVYDKKLEPGPISTINPCPPKEC 233  
Db 198 LQSSGLYSLSSMVTVPGST-SGOTFTCVAHPRASKVDKAVDP----TKRSP-----C 247

Qy 234 HKCPAPNLLEGGSVVFIFPNNIKQVWLMSTLPKVTCVVWDVSEDDPDVQISWVNNEVHT 293  
Db 248 DCCEPPPELPGGSVIFFPKPKDTLTSGTPETCVVWDVGHDPEVKFWVFDVDEVNT 307

Qy 294 AQQTHRDYNSTRVYSTLPOHODMSGKFKCKYNNKDAPSPIRTISKIKGLWRAP 353  
Db 308 ATTKKPREEQFNSTYRVVSAQRLIQHDWKGKKEPKVKNVNEGLPAPIVTRISRKGPAREP 367

Qy 354 QVILPPLPAEQLSRKDVSLSLTCLVWGFNPQDISWEWTSG--HTEENYDAPVLDGSY 411  
Db 368 QVYVLLARPOOEELSKSTVSLTCMVTSPYDVIAVEWORNGOPESDEKDYGTPPOLLADSSY 427

Qy 412 FIVSKLNKNTSKWEKTDSFSCCNVRHREGIKNYVKKTISRSPGK 454  
Db 428 FLYSKLVRDRNSWQEGDITVCMVHEALHNHYTQKSISAGK 470

RESULT 14

G3MSC  
Ig gamma-3 chain C region, secreted form - mouse  
C; Species: Mus musculus (house mouse)  
C; Date: 17-Mar-1987 #sequence\_revision 31-Mar-1991 #text\_change 16-Jul-1999  
C; Accession: B02156  
R; Weis, J.A.; Word, C.J.; Rimm, D.; Der-Balian, G.P.; Martinez, H.M.; Tucker, P.W.; Bl  
EMBO J. 3, 2041-2046, 1984  
A; Title: Structure analysis of the murine IgG3 constant region gene.  
A; Reference number: A02156; MUID:85027161  
A; Accession: B02156  
A; Molecule type: DNA  
A; Residues: 1-329 <WEL>  
A; Cross-references: GB:J00451  
A; Note: the sequence was determined from the germline gene  
C; Genetics:  
A; Gene: Ig gamma-3 chain C region - rat (fragment)  
A; Introns: 97/1; 113/1; 223/1  
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chains disulfide bonded. In some cases, such as IgA and IgM, the subunits associate into C; Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>  
C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl  
F; 19-83/Domain: immunoglobulin homology <IMI>  
F; 97-121/Region: hinge  
F; 136-205/Domain: immunoglobulin homology <IM2>  
F; 179-322/Binding site: carbohydrate (Asn) (covalent) #status predicted  
S00847

Query Match 47.0%; Score 1170; DB 1; Length 329;  
Best Local Similarity 66.2%; Pred. No. 1.1e-62; Mismatches 74; Indels 6; Gaps 1;  
Matches 221; Conservative 33; Mismatches 74;

Qy 121 TPPSVYPLAPGCDITGSSVNLKGYPPESVTVWNSGLSSVHTFALLSGLI 180  
Db 2 TTPPSVYPLAPGCDITGSSVNLKGYPPESVTVWNSGLSSVHTFALLSGLI 181

Qy 181 TMSSSVTVPSPSTNPQSTVTCVASHASSSTVDKLERPSGPISTINPCPCKCHKCPN 240  
Db 62 SLSSLVTVPSWPSQTVICNVAPASKTELKRIEPR----IPRPSTPPSSCPPGN 115

Search completed: June 18, 2001, 15:32:47  
Job time: 165 sec

19 gamma-3 chain C region, membrane-bound form - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 13-Aug-1986 #sequence\_revision 31-Mar-1991 #text\_change 16-Jul-1999  
 C;Accession: A02156; A02155  
 R;Weis, J.A.; Wold, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, P.W.; Blatt  
 REBO J., 3, 2041-2046, 1984  
 A;Title: Structure analysis of the murine IgG3 constant region gene.  
 A;Reference number: A02156; MUID:85027161  
 A;Accession: A02156  
 A;Molecule type: DNA  
 A;Residues: 1-398 <WEL>  
 A;Cross-references: GB:J00451; NID:9194392; PIDN:AAB5655.1; PID:9194433  
 A;Note: the sequence was determined from the germline gene  
 R;Komaromy, M.; Clayton, L.; Rogers, J.; Robertson, S.; Kettman, J.; Wall, R.  
 Nucleic Acids Res. 11, 6775-6785, 1983  
 A;Title: The structure of the mouse immunoglobulin in gamma-3 membrane gene segment.  
 A;Reference number: A02155; MUID:84041483  
 A;Accession: A02155  
 A;Molecule type: DNA  
 A;Residues: 328-332,'G', 334-341,'Q', 343-387,'F', 389-398 <KOM>  
 A;Cross references: GB:K00688  
 A;Note: the sequence was determined from the germline gene  
 C;Genetics:  
 A;Introns: 97/1; 113/1; 223/1; 328/1; 371/3  
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin  
 F;19-83/Domain: immunoglobulin homology <IM1>  
 F;97-112/Region: hinge  
 F;136-205/Domain: immunoglobulin homology <IM2>  
 F;242-309/Domain: immunoglobulin homology <IM3>  
 F;345-362/Domain: transmembrane #status predicted <TM>  
 F;363-398/Domain: intracellular #status predicted <INT>  
 F;179-322/Binding site: carbohydrate (Asn) (covalent) #status predicted

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